```
FILE 'REGISTRY' ENTERED AT 13:31:54 ON 08 APR 2002

=> S RNASE P/CN
L1             1 RNASE P/CN

=> D

L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2002 ACS
RN   71427-00-4  REGISTRY
CN   Nuclease, ribo-, P (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Ribonuclease P
CN     ***RNase P***
MF   Unspecified
CI   MAN
LC   STN Files:   AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CEN,
       CIN, EMBASE, PROMT, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
             738 REFERENCES IN FILE CA (1967 TO DATE)
               8 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
             739 REFERENCES IN FILE CAPLUS (1967 TO DATE)

FILE 'CAPLUS' ENTERED AT 13:32:23 ON 08 APR 2002

=> S RIBONUCLEASE P;S RNASE P;S ANTIBIOTIC;S ANTIBACTERIAL;S CONSENSUS
          11563 RIBONUCLEASE
            999 RIBONUCLEASES
          12162 RIBONUCLEASE
                  (RIBONUCLEASE OR RIBONUCLEASES)
          32247 RNASE
           2308 RNASES
          32759 RNASE
                  (RNASE OR RNASES)
          37318 RIBONUCLEASE
                  (RIBONUCLEASE OR RNASE)
        1964190 P
L2          946 RIBONUCLEASE P
                  (RIBONUCLEASE(W)P)


          32247 RNASE
           2308 RNASES
          32759 RNASE
                  (RNASE OR RNASES)
        1964190 P
L3          929 RNASE P
                  (RNASE(W)P)


          96874 ANTIBIOTIC
          88177 ANTIBIOTICS
L4       131677 ANTIBIOTIC
                  (ANTIBIOTIC OR ANTIBIOTICS)


          58486 ANTIBACTERIAL
           2777 ANTIBACTERIALS
L5        59332 ANTIBACTERIAL
                  (ANTIBACTERIAL OR ANTIBACTERIALS)


          23291 CONSENSUS
             25 CONSENSUSES
L6        23306 CONSENSUS
                  (CONSENSUS OR CONSENSUSES)

=> S L1,L2,L3
            739 L1
L7          955 (L1 OR L2 OR L3)
```

=> S L7 AND L4;S L7 AND L5
L8 14 L7 AND L4

L9 5 L7 AND L5

=> S L8,L9
L10 17 (L8 OR L9)

=> D 1-17 CBIB ABS

L10 ANSWER 1 OF 17 CAPLUS COPYRIGHT 2002 ACS
2002:85514 Inhibition of nuclear pre-mRNA splicing by ***antibiotics*** in vitro. Hertweck, Maren; Hiller, Reinhard; Mueller, Manfred W. (Vienna BioCenter, Institute of Microbiology and Genetics, Vienna, Austria). European Journal of Biochemistry, 269(1), 175-183 (English) 2002. CODEN: EJBCAI. ISSN: 0014-2956. Publisher: Blackwell Publishing Ltd..
AB A no. of ***antibiotics*** have been reported to disturb the decoding process in prokaryotic translation and to inhibit the function of various natural ribozymes. We investigated the effect of several ***antibiotics*** on in vitro splicing of a eukaryotic nuclear pre-mRNA (-globin). Of the eight ***antibiotics*** studied, erythromycin, Cl-tetracycline and streptomycin were identified as splicing inhibitors in nuclear HeLa cell ext. The Ki values were 160, 180 and 230 M, resp. Cl-tetracycline-mediated and streptomycin-mediated splicing inhibition were in the molar inhibition range for hammerhead and human hepatitis delta virus ribozyme self-cleavage (tetracycline), of group-1 intron self-splicing (streptomycin) and inhibition of ***RNase*** ***P*** cleavage by some aminoglycosides. Cl-tetracycline and the aminocyclitol glycoside streptomycin were found to have an indirect effect on splicing by unspecific binding to the pre-mRNA, suggesting that the inhibition is the result of disturbance of the correct folding of the pre-mRNA into the splicing-compatible tertiary structure by the charged groups of these ***antibiotics*** . The macrolide, erythromycin, the strongest inhibitor, had only a slight effect on formation of the presplicing complexes A and B, but almost completely inhibited formation of the splicing-active C complex by binding to nuclear ext. component(s). This results in direct inhibition of the second step of pre-mRNA splicing. To our knowledge, this is the first report on specific inhibition of nuclear splicing by an ***antibiotic*** . The functional groups involved in the interaction of erythromycin with snRNAs and/or splicing factors require further investigation.

L10 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2002 ACS
2001:654730 Document No. 135:223458 Bacterial ***RNase*** ***P*** protein subunits and their use in identifying ***antibacterial*** compounds. Gopalan, Venkat; Jovanovic, Milan; Eder, Paul S.; Giordano, Tony; Powers, Gordon D.; Xavier, K. Asish (Message Pharmaceuticals, Inc., USA; Ohio State University). Eur. Pat. Appl. EP 1130091 A2 20010905, 58 pp. DESIGNATED STATES: R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO. (English). CODEN: EPXXDW. APPLICATION: EP 2001-105007 20010301. PRIORITY: US 2000-516061 20000301.
AB The invention features novel bacterial ***RNase*** ***P*** protein subunits and encoding nucleic acids. The novel ***RNASe*** ***P*** amino acid and nucleic acid sequences were discovered using the genomic database BLAST search of several pathogenic bacteria. Nucleotide and encoded amino acid sequences of the enzymes are disclosed. Methods for discovery of ***antibacterial*** compds. are also featured.

L10 ANSWER 3 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:829933 Document No. 134:110160 Inhibition of eukaryotic ***ribonuclease*** ***P*** activity by aminoglycosides: kinetic studies. Tekos, A.; Tsagla, A.; Stathopoulos, C.; Drainas, D. (School of Medicine, Department of Biochemistry, University of Patras, Patras, 26500, Greece). FEBS Letters, 485(1), 71-75 (English) 2000. CODEN: FEBLAL. ISSN: 0014-5793. Publisher: Elsevier Science B.V..
AB The effect of several aminoglycoside ***antibiotics*** on ***RNase*** ***P*** was investigated using an in vitro exptl. system from Dictyostelium discoideum. Detailed kinetic anal. showed that all aminoglycosides tested (tobramycin, gentamicin, kanamycin, paromomycin, neomycin) behave as classical non-competitive inhibitors, with neomycin

being the strongest inhibitor. The inhibition effect is attributed to the electrostatic competition of the cationic aminoglycosides with magnesium ions required for catalysis. Increasing Mg2+ ion concns. reduced the effect of aminoglycosides on ***RNase*** ***P*** activity. Detailed kinetic anal. showed that aminoglycosides compete with Mg2+ for common binding sites on ***RNase*** ***P*** holoenzyme.

L10 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:824388 Document No. 134:14738 ***RNase*** ***P*** from Staphylococcus aureus and its sequence and solution structure and use for identifying antagonists for treatment of ***antibacterial*** infections. Lehr, Ruth V.; Spitzfaden, Claus; Nicholson, Neville; Jones, Joanna (SmithKline Beecham Corporation, USA; SmithKline Beecham PLC). PCT Int. Appl. WO 2000070025 A1 20001123, 99 pp. DESIGNATED STATES: W: JP, US; RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US13946 20000519. PRIORITY: US 1999-PV134802 19990519; US 1999-PV140044 19990618.
AB This invention relates to a novel bacterial ribonucleoprotein complex and the component parts thereof. More specifically, this invention relates to ***RNase*** ***P*** protein and RNA isolated from Staphylococcus aureus and the use of ***RNase*** ***P*** RNA in screens for the identification of antimicrobial compds. and to the use of such compds. in therapy. The spp gene encoding the protein subunit of S. aureus ***RNase*** ***P*** was cloned and identified on the basis of amino acid sequence homol. with Bacillus subtilis and related bacterial ***RNase*** ***P*** proteins. RNase protein employs 2 different modes of RNA interactions, which occupy distinct areas. NMR spectroscopy identifies a contiguous interaction site for flexible, single-strand RNA mols., representative of the 5'-leader sequence. Binding at this site is dominated by electrostatic charge and hydrogen bonding interactions, including main chain hydrogen bonds at the edge of the .beta.-sheet. The arginine-rich motif of ***RNase*** ***P*** protein does not bind to single-stranded RNA and is therefore likely to be responsible for the binding to the highly structured P RNA component. Given the essentiality of ***RNase*** ***P*** for the viability of the organism, knowledge of the S. aureus protein structure and insight into its interaction with RNA will help in the development of ***RNase*** ***P*** and its protein subunit as targets for novel ***antibiotics*** against this important pathogen.

L10 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:814666 Document No. 133:360470 ***RNase*** ***P*** genes, polypeptides, and RNA from Staphylococcus aureus and their use as ***antibacterial*** targets. Gress, Michael J.; Hegg, Lisa A.; Li, Hu; Park, Joseph J. (Smithkline Beecham Corp., USA; Smithkline Beecham PLC). PCT Int. Appl. WO 2000068430 A1 20001116, 82 pp. DESIGNATED STATES: W: JP, US; RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US12252 20000504. PRIORITY: US 1999-PV133069 19990507.
AB This invention relates to a novel bacterial ***RNase*** ***P*** ribonucleoprotein complex and the component parts thereof from Staphylococcus aureus strain WCUH 29. The ***RNase*** ***P*** protein exhibits greatest homol. over its entire length with the amino acid sequence of Bacillus subtilis protein among known proteins. The effects of buffer conditions, KCl, pH, and MgCl2 on the catalytic properties of S. aureus ***RNase*** ***P*** are characterized. More specifically, this invention relates to ***RNase*** ***P*** RNA isolated from Staphylococcus aureus and the use of ***RNase*** ***P*** RNA in screens for the identification of antimicrobial compds. and to the use of such compds. in therapy.

L10 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:809676 Document No. 134:95170 Effect of peptidyltransferase inhibitors on ***RNase*** ***P*** activity from Dictyostelium discoideum: effect of ***antibiotics*** on ***RNase*** ***P*** . Stathopoulos, Constantinos; Tsagla, Antigoni; Tekos, Apostolos; Drainas, Denis (Department of Biochemistry, School of Medicine, University of Patras, Patras, 26500, Greece). Molecular Biology Reports, 27(2), 107-111 (English) 2000. CODEN: MLBRBU. ISSN: 0301-4851. Publisher: Kluwer Academic Publishers.
AB The effect of several peptidyltransferase inhibitors on ***RNase***

P activity from Dictyostelium discoideum was investigated. Among the inhibitors tested puromycin, amicetin and blasticidin S revealed a dose-dependent inhibition of tRNA maturation. Blasticidin S and amicetin do not compete with puromycin for the same site on the enzyme, suggesting the existence of distinct ***antibiotic*** binding sites on D. discoideum ***RNase*** ***P*** . Inhibition expts. further indicate that binding sites for blasticidin S and amicetin overlap.

L10 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:191198 Document No. 132:248484 A Staphylococcus aureus homolog of the protein moiety of ***ribonuclease*** ***P*** of Bacillus subtilis identified by gene discovery and the development of novel ***antibiotics*** . Guth, Sabine; Jennings, Joanne; Prescott, Catherine D.; Hegg, Lisa A.; Li, Hu (Smithkline Beecham Corporation, USA; Smithkline Beecham, PLC). PCT Int. Appl. WO 2000015775 A1 20000323, 76 pp. DESIGNATED STATES: W: JP; RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US21644 19990917. PRIORITY: US 1998-156145 19980917.
AB The S. aureus homolog of the ***RNase*** ***P*** protein moiety gene spp of B. subtilis is identified by sequence homol. The gene and gene product may of use in diagnosis and identification of the pathogen and in screening and development of novel ***antibiotics*** (no data). The protein was manufd. as a fusion product with maltose-binding protein, release by cleavage with factor Xa and combined with the RNA moiety prepd. by in vitro transcription to give a catalytically active enzyme.

L10 ANSWER 8 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:128642 Document No. 132:259998 Modulation of RNA function by aminoglycoside ***antibiotics*** . Schroeder, Renee; Waldsich, Christina; Wank, Herbert (Vienna Biocenter, Institute of Microbiology and Genetics of the University of Vienna, Vienna, A-1030, Austria). EMBO J., 19(1), 1-9 (English) 2000. CODEN: EMJODG. ISSN: 0261-4189. Publisher: Oxford University Press.
AB A review with many refs. One of the most important families of ***antibiotics*** are the aminoglycosides, including drugs such as neomycin B, paromomycin, gentamicin and streptomycin. With the discovery of the catalytic potential of RNA, these ***antibiotics*** became very popular due to their RNA-binding capacity. They serve for the anal. of RNA function as well as for the study of RNA as a potential therapeutic target. Improvements in RNA structure detn. recently provided first insights into the decoding site of the ribosome at high resoln. and how aminoglycosides might induce misreading of the genetic code. In addn. to inhibiting prokaryotic translation, aminoglycosides inhibit several catalytic RNAs such as self-splicing group I introns, ***RNase*** ***P*** and small ribozymes in vitro. Furthermore, these ***antibiotics*** interfere with human immunodeficiency virus (HIV) replication by disrupting essential RNA-protein contacts. Most exciting is the potential of many RNA-binding ***antibiotics*** to stimulate RNA activities, conceiving small-mol. partners for the hypothesis of an ancient RNA world. SELEX (systematic evolution of ligands by exponential enrichment) has been used in this evolutionary game leading to small synthetic RNAs, whose NMR structures gave valuable information on how aminoglycosides interact with RNA, which could possibly be used in applied science.

L10 ANSWER 9 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:108042 Document No. 132:260232 Inhibition of Dictyostelium discoideum ***ribonuclease*** ***P*** activity by aminoglycosides. Tekos, Apostolos; Tsagla, Antigoni; Stathopoulos, Constantinos; Drainas, Denis (Department of Biochemistry, School of Medicine, University of Patras, Patras, 26500, Greece). Nucleic Acids Symp. Ser., 41(Symposium on RNA Biology III: RNA, Tool & Target), 152-154 (English) 1999. CODEN: NACSD8. ISSN: 0261-3166. Publisher: Oxford University Press.
AB The effect of several aminoglycoside ***antibiotics*** on ***RNase*** ***P*** (***RNase*** ***P***) was investigated using an in vitro exptl. system from Dictyostelium discoideum. All aminoglycosides tested (tobramycin, gentamycin, kanamycin, paromomycin, neomycin) revealed a dose-dependent inhibition of tRNA maturation, indicating that they may have a direct effect on tRNA biogenesis. Neomycin, an aminoglycoside highly substituted by amino groups, is the strongest inhibitor indicating that the amt. of pos. charges may play a

crucial role for the ***antibiotic*** action. Evidence is presented that the inhibition effect may be attributed to the electrostatic competition of the cationic aminoglycosides with magnesium ions required for catalysis.

L10 ANSWER 10 OF 17 CAPLUS COPYRIGHT 2002 ACS
2000:12468 Document No. 132:191166 The Structure of ***Ribonuclease*** ***P*** Protein from Staphylococcus aureus Reveals a Unique Binding Site for Single-stranded RNA. Spitzfaden, Claus; Nicholson, Neville; Jones, Jo J.; Guth, Sabine; Lehr, Ruth; Prescott, Cathy D.; Hegg, Lisa A.; Eggleston, Drake S. (Computational and Structural Sciences, SmithKline Beecham Pharmaceuticals, Harlow, CM19 5AW, UK). J. Mol. Biol., 295(1), 105-115 (English) 2000. CODEN: JMOBAK. ISSN: 0022-2836. Publisher: Academic Press.
AB ***RNase*** ***P*** (RNaseP) catalyzes the removal of the 5'-leader sequence from pre-tRNA to produce the mature 5' terminus. The prokaryotic RNaseP holoenzyme consists of a catalytic RNA component and a protein subunit (RNaseP protein), which plays an auxiliary but essential role in vivo by binding to the 5'-leader sequence and broadening the substrate specificity of the ribozyme. We detd. the three-dimensional high-resoln. structure of the RNaseP protein from Staphylococcus aureus (117 amino acid residues) by NMR spectroscopy in soln. The protein has an .alpha..beta.-fold, similar to the ribonucleoprotein domain. We used small nucleic acid mols. as a model for the 5'-leader sequence to probe the propensity for generic single-stranded RNA binding on the protein surface. The NMR results reveal a contiguous interaction site, which is identical with the previously identified leader sequence binding site in RNaseP holoenzyme. The conserved arginine-rich motif does not bind single-stranded RNA. It is likely that this peptide segment binds selectively to double-stranded sections of P RNA, which are conformationally more rigid. Given the essentiality of RNaseP for the viability of the organism, knowledge of the S. aureus protein structure and insight into its interaction with RNA will help us to develop RNaseP and RNaseP protein as targets for novel ***antibiotics*** against this pathogen. (c) 2000 Academic Press.

L10 ANSWER 11 OF 17 CAPLUS COPYRIGHT 2002 ACS
1999:456714 Document No. 131:226001 Inhibition of ***RNase*** ***P*** RNA cleavage by aminoglycosides. Mikkelsen, Nils E.; Brannvall, Mathias; Virtanen, Anders; Kirsebom, Leif A. (Department of Cell and Molecular Biology, Biomedical Center, Uppsala University, Uppsala, SE-751 24, Swed.). Proc. Natl. Acad. Sci. U. S. A., 96(11), 6155-6160 (English) 1999. CODEN: PNASA6. ISSN: 0027-8424. Publisher: National Academy of Sciences.
AB A no. of aminoglycosides have been reported to interact and interfere with the function of various RNA mols. Among these are 16S rRNA, the group I intron, and the hammerhead ribozymes. In this report we show that cleavage by ***RNase*** ***P*** RNA in the absence as well as in the presence of the ***RNase*** ***P*** protein is inhibited by several aminoglycosides. Among the ones we tested, neomycin B was the strongest inhibitor with a Ki value in the micromolar range (35 .mu.M). Studies of lead(II)-induced cleavage of ***RNase*** ***P*** RNA suggested that binding of neomycin B interfered with the binding of divalent metal ions to the RNA. Taken together, our findings suggest that aminoglycosides compete with Mg2+ ions for functionally important divalent metal ion binding sites. Thus, ***RNase*** ***P*** , which is an essential enzyme, is indeed a potential drug target that can be used to develop new drugs by using various aminoglycosides as lead compds.

L10 ANSWER 12 OF 17 CAPLUS COPYRIGHT 2002 ACS
1998:793064 Document No. 130:35133 P-selectin translocation to vascular epithelial lumen by ionizing radiation, and therapeutic use. Hallahan, Dennis E.; Virudachalam, Subbulakshmi (Arch Development Corporation, USA). PCT Int. Appl. WO 9853852 A1 19981203, 178 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1998-US10913

19980529. PRIORITY: US 1997-48141 19970530.

AB The present invention relates to the use of P-selectin as a targeting agent in radiotherapies for vascular related disease. P-selectin is translocated to the lumen of vascular endothelia as a result of radiation. Thus, P-selecting provides a target for receptor-mediated delivery of drugs, including anticancer drugs and drugs for the treatment of vascular disease. However, P-selectin also plays a role in the activation of certain inflammatory cells and, as such, plays a role in radiation-induced inflammation. By interfering with P-selectin induction of inflammation, it is possible to modulate inflammatory responses to radiation therapy.

L10 ANSWER 13 OF 17 CAPLUS COPYRIGHT 2002 ACS

1998:131142 Document No. 128:208891 Drug-sensitive phenotypic conversion of resistant cells mediated by external guide nucleotide sequences. Takle, Garry B.; Goldberg, Allan R.; George, Shaji T. (Innovir Laboratories, Inc., USA). PCT Int. Appl. WO 9806440 A2 19980219, 63 pp. DESIGNATED STATES: W: AU, CA, JP; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1997-US14457 19970815. PRIORITY: US 1996-23675 19960816.

AB Disclosed are a method and compns. for delivering nucleic acids to bacterial cells. The method does not require manipulation of the bacteria and is therefore particularly suited to delivery of nucleic acids to bacteria in natural environments, including inside animal bodies. The method generally involves conjugating the nucleic acid to be delivered with a cationic porphyrin and bringing the conjugate and the target bacterial cells into contact. Both the porphyrin and conjugated nucleic acid are taken up by the bacterial cells and the nucleic acid can then have a biol. effect on the cells. Specifically disclosed is a method for converting drug-resistant bacterial cells to drug-sensitive cells by delivery of external guide sequences to the cells which then promote cleavage of RNA mols. involved in conferring the drug-resistant phenotype on the cells. The drug-resistant phenotype of the cells is thus converted to a drug-sensitive phenotype. The drug-sensitive cells are then susceptible to drug therapy. Also disclosed is a method and compns. for killing eukaryotic pathogens or converting drug-resistant eukaryotic cells to drug-sensitive cells. The method involves the delivery of external guide sequences, ribozymes, or vectors encoding external guide sequences or ribozymes, to eukaryotic cells. Preferred target eukaryotic cells for the disclosed method include algae, protozoa, fungi, slime mold, and cells of helminths.

L10 ANSWER 14 OF 17 CAPLUS COPYRIGHT 2002 ACS

1998:126347 Document No. 128:188619 Phenotypic conversion of drug-resistant bacteria to drug-sensitivity using external guide sequences to promote RNase cleavage of ***antibiotic*** resistance-conferring RNA. Altman, Sidney; Guerrier-Takada, Cecilia L. (Yale University, USA). PCT Int. Appl. WO 9806837 A1 19980219, 35 pp. DESIGNATED STATES: W: AU, CA, JP; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1997-US14455 19970815. PRIORITY: US 1996-23675 19960816; US 1997-53774 19970725.

AB External guide sequences ("EGS") can be used to promote ***RNase*** ***P*** -mediated cleavage of RNA transcribed from plasmids and other genetic elements which confer drug resistance on bacterial cells. Such cleavage can render the bacteria drug sensitive. The EGS comprises an oligonucleotide having at its 5'-terminus nucleotides complementary to the nucleotides 3' to a specific cleavage site in an ***antibiotic*** -resistance-conferring RNA mol. to be cleaved, and at its 3'-terminus the nucleotides NCCA joined to the complementary nucleotides. In a preferred embodiment, a vector encoding an EGS is administered to an animal or human harboring ***antibiotic*** resistant bacterial cells such that the EGS is expressed in the bacterial cells, the EGS promotes ***RNase*** ***P*** -mediated cleavage of RNA involved in conferring ***antibiotic*** resistance to the cells, and the cells are rendered ***antibiotic*** sensitive. A preferred form of administration is via inoculation of the animal or human with cells contg. genes for appropriate EGSs on promiscuous plasmids. These plasmids will spread quickly through the ***antibiotic*** -resistant population of bacterial cells, thereby making the cells susceptible to ***antibiotic*** therapy. Thus, synthetic genes coding for EGSs were inserted into plasmids compatible with other plasmids bearing drug resistance genes in Escherichia coli. The EGSs, designed to form complexes with mRNA encoded by genes for either

ampicillin or chloramphenicol resistance, direct ***RNase*** ***P*** to cleave the targeted mRNAs, thereby converting the phenotype of drug-resistance cells to drug-sensitivity.

L10 ANSWER 15 OF 17 CAPLUS COPYRIGHT 2002 ACS
1997:803728 Document No. 128:85173 Cloning and characterization of Staphylococcus aureus ***RNase*** ***P*** . Guth, Sabine; Prescott, Catherine D.; Jennings, Joanne (Smithkline Beecham Corporation, USA; Smithkline Beecham PLC). Eur. Pat. Appl. EP 811688 A2 19971210, 51 pp. DESIGNATED STATES: R: BE, CH, DE, DK, FR, GB, IT, LI, NL. (English). CODEN: EPXXDW. APPLICATION: EP 1997-303918 19970606. PRIORITY: US 1996-19234 19960606; US 1996-29928 19961101; US 1996-29929 19961101.
AB This invention relates to a novel bacterial ribonucleoprotein complex and the component parts thereof. The genes for the protein and catalytic RNA components of S. aureus ***RNase*** ***P*** are provided. More specifically, this invention relates to ***RNase*** ***P*** isolated from Staphylococcus aureus and the use of ***RNase*** ***P*** or components thereof in screens for the identification of antimicrobial compds. and to the use of such compds. in therapy.

L10 ANSWER 16 OF 17 CAPLUS COPYRIGHT 2002 ACS
1997:531189 Document No. 127:231795 Phenotypic conversion of drug-resistant bacteria to drug sensitivity. Guerrier-Takada, Cecilia; Salavati, Reza; Altman, Sidney (Department of Biology, Yale University, New Haven, CT, 06520, USA). Proc. Natl. Acad. Sci. U. S. A., 94(16), 8468-8472 (English) 1997. CODEN: PNASA6. ISSN: 0027-8424. Publisher: National Academy of Sciences.
AB Plasmids that contain synthetic genes coding for small oligoribonucleotides called external guide sequences (EGSs) have been introduced into strains of Escherichia coli harboring ***antibiotic*** resistance genes. The EGSs direct ***RNase*** ***P*** to cleave the mRNAs transcribed from these genes, thereby converting the phenotype of drug-resistant cells to drug sensitivity. Increasing the EGS-to-target mRNA ratio by changing gene copy no. or the no. of EGSs complementary to different target sites enhances the efficiency of the conversion process.

L10 ANSWER 17 OF 17 CAPLUS COPYRIGHT 2002 ACS
1993:644156 Document No. 119:244156 RNase MRP and ***RNase*** ***P*** share a common substrate. Potuschak, Thomas; Rossmanith, Walter; Karwan, Robert (Inst. Tumorbiol. Krebsforsch., Univ. Wien, Vienna, A-1090, Austria). Nucleic Acids Res., 21(14), 3239-43 (English) 1993. CODEN: NARHAD. ISSN: 0305-1048.
AB RNase MRP is a site-specific ribonucleoprotein endoribonuclease that processes RNA from the mammalian mitochondrial displacement loop-contg. region. ***RNase*** ***P*** is a site-specific ribonucleoprotein endoribonuclease that processes pre-tRNAs to generate their mature 5'-ends. A similar structure for the ***RNase*** ***P*** and RNase MRP RNAs and a common cleavage mechanism for RNase MRP and ***RNase*** ***P*** enzymes have been proposed. Expts. with protein synthesis ***antibiotics*** showed that both RNase MRP and ***RNase*** ***P*** were inhibited by puromycin. Here, it is also shown that E. coli ***RNase*** ***P*** cleaves the RNase MRP substrate, mouse mitochondrial primer RNA, exactly at a site that is cleaved by RNase MRP.

=> S L7 AND L6
L11 27 L7 AND L6

=> S L11 NOT L10
L12 27 L11 NOT L10

=> S STRUCTURE;S L6(W)L13
2103158 STRUCTURE
553179 STRUCTURES
L13 2363545 STRUCTURE
(STRUCTURE OR STRUCTURES)

L14 91 L6(W)L13

=> S L14 AND L7
L15 4 L14 AND L7

=> D 1-4 CBIB ABS

L15 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2002 ACS
2001:537972 Document No. 135:223233 The first phytoplasma ***RNase*** ***P*** RNA provides new insights into the sequence requirements of this ribozyme. Wagner, Matthias; Fingerhut, Christiane; Gross, Hans J.; Schon, Astrid (Institut for Biochemie, Bayerische Julius-Maximilians-Universitat, Wurzburg, D-97074, Germany). Nucleic Acids Research, 29(12), 2661-2665 (English) 2001. CODEN: NARHAD. ISSN: 0305-1048. Publisher: Oxford University Press.
AB A high variability of ***RNase*** ***P*** RNA structures is seen among members of the Mycoplasma group. To gain further insight into the structure-function relations of this ribozyme, we have searched for the ***RNase*** ***P*** RNA gene from more distant relatives, the phytoplasmas. These mycoplasma-like organisms are the etiol. agents of many severe plant diseases. We report the sequence and catalytic properties of ***RNase*** ***P*** RNA from the phytoplasma causing apple proliferation disease. The primary and postulated secondary structure of this 443 nt long RNA are most similar to those of Acholeplasma, supporting the phylogenetic position of this pathogen. Remarkably, the extremely AT-rich (73.6%) phytoplasma RNA differs from the known bacterial consensus sequence by a single base pair, which is positioned close to the substrate cleavage site in current three-dimensional models. Phytoplasma ***RNase*** ***P*** RNA functions as an efficient ribozyme in vitro. Conversion of its sequence to the full consensus and kinetic anal. of the resulting mutant RNAs suggests that neither the sequence alone, nor the type of pairing at this position is crucial for substrate binding or catalysis by the ***RNase*** ***P*** ribozyme. These results refine the bacterial ***consensus*** ***structure*** close to the catalytic core and thus improve our understanding of ***RNase*** ***P*** RNA function.

L15 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS
1999:570696 Document No. 132:74094 A comparative genomics approach to the evolution of eukaryotes and their mitochondria. Lang, B. Franz; Seif, Elias; Gray, Michael W.; O'Kelly, Charles J.; Burger, Gertraud (Departement de biochimie, Universite de Montreal, Montreal, QC, H3C 3J7, Can.). Journal of Eukaryotic Microbiology, 46(4), 320-326 (English) 1999. CODEN: JEMIED. ISSN: 1066-5234. Publisher: Society of Protozoologists.
AB The Organelle Genome Megasequencing Program (OGMP) investigates mitochondrial genome diversity and evolution by systematically detg. the complete mitochondrial DNA (mtDNA) sequences of a phylogenetically broad selection of protists. The mtDNAs of lower fungi and choanoflagellates are being analyzed by the Fungal Mitochondrial Genome Project (FMGP), a sister project to the OGMP. Some of the most interesting protists include the jakobid flagellates Reclinomonas americana, Malawimonas jakobiformis, and Jakoba libera, which share ultrastructural similarities with amitochondriate retortamonads, and harbor mitochondrial genes not seen before in mtDNAs of other organisms. In R. americana and J. libera, gene clusters are found that resemble, to an unprecedented degree, the contiguous ribosomal protein operons str, S10, spc, and alpha of eubacteria. In addn., their mtDNAs code for an ***RNase*** ***P*** RNA that displays all the elements of a bacterial min. ***consensus*** ***structure*** . This structure has been instrumental in detecting the rnpB gene in addnl. protists. Gene repertoire and gene order comparisons as well as multiple-gene phylogenies support the view of a single endosymbiotic origin of mitochondria, whose closest extant relatives are Rickettsia-type .alpha.-Proteobacteria.

L15 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2002 ACS
1995:119310 Document No. 122:4298 The ***ribonuclease*** ***P*** database. Brown, James W.; Haas, Elizabeth S.; Gilbert, Donald G.; Pace, Norman R. (Dep. Microbiology, North Carolina State Univ., Raleigh, NC, 27695, USA). Nucleic Acids Res., 22(17), 3660-2 (English) 1994. CODEN: NARHAD. ISSN: 0305-1048.
AB The ***RNase*** ***P*** Sequence database is a compilation of ***RNase*** ***P*** sequences, sequence alignments, secondary structures, three-dimensional models, and accessory information. In its

initial form, the database contains information on ***RNase*** ***P*** RNA in bacteria and archaea, and ***RNase*** ***P*** protein in bacteria. The sequences themselves are presented phylogenetically ordered and aligned. The database also contains secondary structures of bacterial and archaeal RNAs, including specially annotated 'ref.' secondary structures of Escherichia coli and Bacillus subtilis ***RNase*** ***P*** , RNAs, a min. phylogenetic ***consensus*** ***structure*** , and coordinates for models of three-dimensional structure.

L15 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS
1993:533772 Document No. 119:133772 Comparative structural analysis of nuclear ***RNase*** ***P*** RNAs from yeast. Tranguch, Anthony J.; Engelke, David R. (Dep. Biol. Chem., Univ. Michigan, Ann Arbor, MI, 48109-0606, USA). J. Biol. Chem., 268(19), 14045-55 (English) 1993. CODEN: JBCHA3. ISSN: 0021-9258.
AB Secondary structure models for yeast nuclear ***RNase*** ***P*** RNAs were derived by phylogenetic comparative anal. ***RNase*** ***P*** RNA genes from six Saccharomyces species were characterized and compared with the published gene sequences of Saccharomyces cerevisiae (RPR1), Schizosaccharomyces pombe, and Schizosaccharomyces octosporus. The general organization of the Saccharomyces genes were similar; all were present in single copy and contained RNA polymerase III-specific regulatory elements, including tRNA gene-like A- and B-box promoters located within 5' leader regions and poly(T) terminators following the mature RNA domains. As obsd. previously, two ***RNase*** ***P*** RNAs were present in each of the species: a shorter RNA corresponding to the mature domain and a longer possible precursor RNA that includes the 5' leader sequences. The mature RNA domains of three of these genes were sufficiently divergent from the S. cerevisiae RNA such that compensatory base changes in paired elements were readily identified, yet homologous regions could be aligned. A striking common core of primary and secondary structure emerged from the Saccharomyces ***RNase*** ***P*** RNAs. Furthermore, the Schizosaccharomyces homologs conformed in large part to the Saccharomyces conserved core and shared with it a distinctive structural domain that has so far only been obsd. in the yeast nuclear ***RNase*** ***P*** RNAs. Comparison of the yeast core to a previously published eubacterial conserved core and to the RNA homologs from vertebrates revealed a no. of similarities, suggesting that ***RNase*** ***P*** RNA from diverse sources may share a core of structurally conserved elements.

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=> S L15 NOT L10
L16          4 L15 NOT L10

=> E GOPALAN V/AU
=> S L3-E7
          7945 'L3'
          3677 E7
L17          0 L3-E7
                 ('L3'(W)E7)

=> S E3-E7
             8 "GOPALAN V"/AU
            14 "GOPALAN VENKAT"/AU
             8 "GOPALAN VENKATAKRISHNAN"/AU
            46 "GOPALAN VENKATRAMAN"/AU
             1 "GOPALAN VERKATRAMAN"/AU
L18         77 ("GOPALAN V"/AU OR "GOPALAN VENKAT"/AU OR "GOPALAN VENKATAKRISHN
               AN"/AU OR "GOPALAN VENKATRAMAN"/AU OR "GOPALAN VERKATRAMAN"/AU)

=> E JOVANOVIC M/AU
=> S E3,E27-E31
           130 "JOVANOVIC M"/AU
            30 "JOVANOVIC MILAN"/AU
             1 "JOVANOVIC MILAN K"/AU
            44 "JOVANOVIC MILAN M"/AU
             1 "JOVANOVIC MILAN R"/AU
             5 "JOVANOVIC MILAN T"/AU
L19        211 ("JOVANOVIC M"/AU OR "JOVANOVIC MILAN"/AU OR "JOVANOVIC MILAN
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               K"/AU OR "JOVANOVIC MILAN M"/AU OR "JOVANOVIC MILAN R"/AU OR
               "JOVANOVIC MILAN T"/AU)

=> E EDER P/AU
=> S E3,E4,E7
             1 "EDER P"/AU
             2 "EDER P S"/AU
            16 "EDER PAUL S"/AU
L20         19 ("EDER P"/AU OR "EDER P S"/AU OR "EDER PAUL S"/AU)

=> E GIORDANO T/AU
=> S E3,E12
             6 "GIORDANO T"/AU
            30 "GIORDANO TONY"/AU
L21         36 ("GIORDANO T"/AU OR "GIORDANO TONY"/AU)

=> E POWERS G/AU
=> S E3,E5,E34,E35
             2 "POWERS G"/AU
             2 "POWERS G D"/AU
             2 "POWERS GORDON"/AU
            10 "POWERS GORDON D"/AU
L22         16 ("POWERS G"/AU OR "POWERS G D"/AU OR "POWERS GORDON"/AU OR "POWE
               RS GORDON D"/AU)

=> E XAVIER K/AU
=> S E4
L23          1 "XAVIER K A"/AU

=> E XAVIER A/AU
=> S E32
L24          1 "XAVIER ASISH K"/AU

=> S L18-L24
L25        349 (L18 OR L19 OR L20 OR L21 OR L22 OR L23 OR L24)

=> S L25 AND L7
L26         14 L25 AND L7

=> S L26 NOT (L10 OR L16)
L27         13 L26 NOT (L10 OR L16)

=> D 1-13 CBIB ABS

L27  ANSWER 1 OF 13  CAPLUS  COPYRIGHT 2002 ACS
2002:209542    ***RNase***     ***P***  : variations and uses.    ***Gopalan,***
  ***     Venkat***  ; Vioque, Agustin; Altman, Sidney (Department of Biochemistry,
     Ohio State University, Columbus, OH, 43210-1292, USA).  Journal of
     Biological Chemistry, 277(9), 6759-6762 (English) 2002.  CODEN: JBCHA3.
     ISSN: 0021-9258.  Publisher: American Society for Biochemistry and
     Molecular Biology.
AB   Unavailable

L27  ANSWER 2 OF 13  CAPLUS  COPYRIGHT 2002 ACS
2002:89366  Inhibition of bacterial   ***RNase***     ***P***   by
     aminoglycoside-arginine conjugates.  Eubank, Timothy D.; Biswas, Roopa;
       ***Jovanovic, Milan***  ; Litovchick, Alexander; Lapidot, Aviva;
       ***Gopalan, Venkat***   (Department of Biochemistry, The Ohio State
     University, Columbus, OH, 43210, USA).  FEBS Letters, 511(1-3), 107-112
     (English) 2002.  CODEN: FEBLAL.  ISSN: 0014-5793.  Publisher: Elsevier
     Science B.V..
AB   The potential of RNAs and RNA-protein (RNP) complexes as drug targets is
     currently being explored in various investigations.  For example, a
     hexa-arginine deriv. of neomycin (NeoR) and a tri-arginine deriv. of
     gentamicin (R3G) were recently shown to disrupt essential RNP interactions
     between the trans-activator protein (Tat) and the Tat-responsive RNA
     (trans-activating region) in the human immunodeficiency virus (HIV) and
     also inhibit HIV replication in cell culture.  Based on certain structural
     similarities, we postulated that NeoR and R3G might also be effective in
     disrupting RNP interactions and thereby inhibiting bacterial   ***RNase***
       ***P***  , an essential RNP complex involved in tRNA maturation.  Our
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results indicate that indeed both NeoR and R3G inhibit ***RNase*** ***P*** activity from evolutionarily divergent pathogenic bacteria and do so more effectively than they inhibit partially purified human ***RNase*** ***P*** activity.

L27 ANSWER 3 OF 13 CAPLUS COPYRIGHT 2002 ACS
2001:211851 Document No. 134:350214 Cleavage of bipartite substrates by rice and maize ***ribonuclease*** ***P*** . Application to degradation of target mRNAs in plants. Raj, M. L. Stephen; Pulukkunat, Dileep K.; Reckard, James F., III.; Thomas, George; ***Gopalan, Venkat*** (Department of Biochemistry, The Ohio State University, Columbus, OH, 43210, USA). Plant Physiology, 125(3), 1187-1190 (English) 2001. CODEN: PLPHAY. ISSN: 0032-0889. Publisher: American Society of Plant Physiologists.
AB A method was developed in order to use ***RNase*** ***P*** for cleaving mRNAs and thereby disrupting gene expression in plants. RNA substrates were designed with a precursor tRNA-like structure and included an external guide sequence (EGS). The ***Rnase*** ***P*** -mediated approach for studying gene function in plants will depend on (a) stable expression of the EGSs, (b) colocalization of the target mRNA substrate and the EGS within the same subcellular compartment, and (c) accessibility of the target mRNA to the EGS.

L27 ANSWER 4 OF 13 CAPLUS COPYRIGHT 2002 ACS
2000:906840 Document No. 134:174599 Varieties of ***RNase*** ***P*** : a nomenclature problem?. Altman, Sidney; ***Gopalan, Venkat*** ; Vioque, Agustin (Department of Molecular, Cellular and Developmental Biology, Yale University, New Haven, CT, 06511, USA). RNA, 6(12), 1689-1694 (English) 2000. CODEN: RNARFU. ISSN: 1355-8382. Publisher: Cambridge University Press.
AB A review, with 48 refs., on eubacterial ***RNase*** ***P*** , archaeal and eukaryal ***RNase*** ***P*** , organellar ***RNase*** ***P*** , and evolution and implications for nomenclature.

L27 ANSWER 5 OF 13 CAPLUS COPYRIGHT 2002 ACS
2000:83019 Document No. 132:305090 Mapping RNA-Protein Interactions in ***Ribonuclease*** ***P*** from Escherichia coli using Disulfide-linked EDTA-Fe. Biswas, Roopa; Ledman, David W.; Fox, Robert O.; Altman, Sidney; ***Gopalan, Venkat*** (Department of Biochemistry, The Ohio State University, Columbus, OH, 43210, USA). J. Mol. Biol., 296(1), 19-31 (English) 2000. CODEN: JMOBAK. ISSN: 0022-2836. Publisher: Academic Press.
AB The protein subunit of Escherichia coli ***RNase*** ***P*** (which has a cysteine residue at position 113) and its single cysteine-substituted mutant derivs. (S16C/C113S, K54C/C113S and K66C/C113S) have been modified using a sulfhydryl-specific iron complex of EDTA-2- aminoethyl 2-pyridyl disulfide (EPD-Fe). This reaction converts C5 protein, or its single cysteine-substituted mutant derivs., into chem. nucleases which are capable of cleaving the cognate RNA ligand, M1 RNA, the catalytic RNA subunit of E. coli ***RNase*** ***P*** , in the presence of ascorbate and hydrogen peroxide. Cleavages in M1 RNA are expected to occur at positions proximal to the site of contact between the modified residue (in C5 protein) and the ribose units in M1 RNA. When EPD-Fe was used to modify residue Cys16 in C5 protein, hydroxyl radical-mediated cleavages occurred predominantly in the P3 helix of M1 RNA present in the reconstituted holoenzyme. C5 Cys54-EDTA-Fe produced cleavages on the 5' strand of the P4 pseudoknot of M1 RNA, while the cleavages promoted by C5 Cys66-EDTA-Fe were in the loop connecting helixes P18 and P2 (J18/2) and the loop (J2/4) preceding the 3' strand of the P4 pseudoknot. However, hydroxyl radical-mediated cleavages in M1 RNA were not evident with Cys113-EDTA-Fe, perhaps indicative of Cys113 being distal from the RNA-protein interface in the ***RNase*** ***P*** holoenzyme. Our directed hydroxyl radical-mediated footprinting expts. indicate that conserved residues in the RNA and protein subunit of the ***RNase*** - ***P*** holoenzyme are adjacent to each other and provide structural information essential for understanding the assembly of ***RNase*** ***P*** . (c) 2000 Academic Press.

L27 ANSWER 6 OF 13 CAPLUS COPYRIGHT 2002 ACS
1999:115458 Document No. 130:322196 Rpp14 and Rpp29, two protein subunits of

human ***ribonuclease*** ***P*** . Jarrous, Nayer; ***Eder, Paul*** *** S.*** ; Wesolowski, Donna; Altman, Sidney (Department of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, CT, 06520, USA). RNA, 5(2), 153-157 (English) 1999. CODEN: RNARFU. ISSN: 1355-8382. Publisher: Cambridge University Press.

AB In HeLa cells, the tRNA processing enzyme ***RNase*** ***P*** consists of an RNA mol. assocd. with at least eight protein subunits, hPop1, Rpp14, Rpp20, Rpp25, Rpp29, Rpp30, Rpp38, and Rpp40. Five of these proteins (hPop1p, Rpp20, Rpp30, Rpp38, and Rpp40) have been partially characterized. Here we report on the cDNA cloning and immunobiochem. anal. of Rpp14 and Rpp29. Polyclonal rabbit antibodies raised against recombinant Rpp14 and Rpp29 recognize their corresponding antigens in HeLa cells and ppt. catalytically active ***RNase*** ***P*** . Rpp29 shows 23% identity with Pop4p, a subunit of yeast nuclear ***RNase*** ***P*** and the rRNA processing enzyme RNase MRP. Rpp14, by contrast, exhibits no significant homol. to any known yeast gene. Thus, human ***RNase*** ***P*** differs in the details of its protein compn., and perhaps in the functions of some of these proteins, from the yeast enzyme.

L27 ANSWER 7 OF 13 CAPLUS COPYRIGHT 2002 ACS

1999:44191 Document No. 130:233948 Mapping RNA-Protein Interactions in ***Ribonuclease*** ***P*** from Escherichia coli Using Electron Paramagnetic Resonance Spectroscopy. ***Gopalan, Venkat*** ; Kuehne, Henriette; Biswas, Roopa; Li, Huimei; Brudvig, Gary W.; Altman, Sidney (Departments of Biology Molecular Biophysics Biochemistry and Chemistry, Yale University, New Haven, CT, 06520, USA). Biochemistry, 38(6), 1705-1714 (English) 1999. CODEN: BICHAW. ISSN: 0006-2960. Publisher: American Chemical Society.

AB ***RNase*** ***P*** is a catalytic ribonucleoprotein (RNP) essential for tRNA biosynthesis. In Escherichia coli, this RNP complex is composed of a catalytic RNA subunit, M1 RNA, and a protein cofactor, C5 protein. Using the sulfhydryl-specific reagent (1-oxyl-2,2,5,5-tetramethyl-.DELTA.3-pyrroline-3-methyl)methanethiosulfonate (MTSL), we have introduced a nitroxide spin label individually at six genetically engineered cysteine residues (i.e., positions 16, 21, 44, 54, 66, and 106) and the native cysteine residue (i.e., position 113) in C5 protein. The spin label covalently attached to any protein is sensitive to structural changes in its microenvironment. Therefore, we expected that if the spin label introduced at a particular position in C5 protein was present at the RNA-protein interface, the ESR spectrum of the spin label would be altered upon binding of the spin-labeled C5 protein to M1 RNA. The EPR spectra obsd. with the various MTSL-modified mutant derivs. of C5 protein indicate that the spin label attached to the protein at positions 16, 44, 54, 66, and 113 is immobilized to varying degrees upon addn. of M1 RNA but not in the presence of a catalytically inactive, deletion deriv. of M1 RNA. In contrast, the spin label attached to position 21 displays an increased mobility upon binding to M1 RNA. The results from this EPR spectroscopy-based approach together with those from earlier studies identify residues in C5 protein which are proximal to M1 RNA in the ***RNase*** ***P*** holoenzyme complex.

L27 ANSWER 8 OF 13 CAPLUS COPYRIGHT 2002 ACS

1998:245969 Document No. 129:38040 Autoantigenic properties of some protein subunits of catalytically active complexes of human ***ribonuclease*** ***P*** . Jarrous, Nayef; ***Eder, Paul S.*** ; Guerrier-Takada, Cecilia; Hoog, Christer; Altman, Sidney (Department of Biology, Yale University, New Haven, CT, 06520, USA). RNA, 4(4), 407-417 (English) 1998. CODEN: RNARFU. ISSN: 1355-8382. Publisher: Cambridge University Press.

AB At least six proteins co-purify with human ***RNase*** ***P*** , a tRNA processing ribonucleoprotein. Two of these proteins, Rpp30 and Rpp38, are Th autoantigens. Recombinant Rpp30 and Rpp38 are also recognized by Th sera from systemic sclerosis patients. Two of the other proteins assocd. with ***RNase*** ***P*** , Rpp20 and Rpp40, do not cross-react with Th sera. Polyclonal antibodies raised against all four recombinant proteins recognize the corresponding proteins assocd. with ***RNase*** ***P*** and ppt. active holoenzyme. Catalytically active ***RNase*** ***P*** holoenzyme can be sepd. from the nucleolar and mitochondrial RNA processing endoribonuclease, RNase MRP, even though these two enzymes may share some subunits.

L27 ANSWER 9 OF 13 CAPLUS COPYRIGHT 2002 ACS
1997:291491 Document No. 126:340405 Analysis of the functional role of conserved residues in the protein subunit of ***ribonuclease*** ***P*** from Escherichia coli. ***Gopalan, Venkat*** ; Basevanis, Andreas D.; Landsman, David; Altman, Sidney (Dep. Bio., Yale Univ., New Haven, CT, 06520-8103, USA). J. Mol. Biol., 267(4), 818-829 (English) 1997. CODEN: JMOBAK. ISSN: 0022-2836. Publisher: Academic.
AB The processing of precursor tRNAs and some other small cellular RNAs by M1 RNA, the catalytic subunit of E. coli ***RNase*** ***P*** , is accelerated by C5 protein (the protein cofactor) both in vitro and in vivo. In the effort to understand the mechanism by which the protein cofactor promotes and stabilizes certain conformations of M1 RNA that are most efficient for ***RNase*** ***P*** catalysis, we have used site-directed mutagenesis to generate mutant derivs. of C5 protein and assessed their ability to promote ***RNase*** ***P*** catalysis in vivo and in vitro. Our results indicate that certain conserved hydrophobic and basic residues in C5 protein are important for its function and that single amino acid residue changes in C5 protein can alter the substrate specificity of the ***RNase*** ***P*** holoenzyme.

L27 ANSWER 10 OF 13 CAPLUS COPYRIGHT 2002 ACS
1997:291370 Document No. 126:340404 Fluorescence properties of a tryptophan residue in an aromatic core of the protein subunit of ***ribonuclease*** ***P*** from Escherichia coli. ***Gopalan, Venkat*** ; Golbik, Ralph; Scheriber, Gideon; Fersht, Alan R.; Altman, Sidney (Dep. Bio., Yale Univ., New Haven, CT, 06520-8103, USA). J. Mol. Biol., 267(4), 765-769 (English) 1997. CODEN: JMOBAK. ISSN: 0022-2836. Publisher: Academic.
AB Escherichia coli ***RNase*** ***P*** (***RNase*** ***P***), a ribonucleoprotein complex which primarily functions in tRNA biosynthesis, is composed of a catalytic RNA subunit, M1 RNA, and a protein cofactor, C5 protein. The fluorescence emission spectrum of the single tryptophan residue-contg. C5 protein exhibits maxima at 318 nm and 332 nm. Based on a comparison of the emission spectra of wild-type C5 protein and some of its mutant derivs., we have detd. that the 318 nm max. could be the result of a complex formed in the excited state as a result of hydrophobic interactions between Trp109, Phe18 and Phe73. The analogous tryptophan fluorescence emission spectra of wild-type C5 protein and the barstar mutant W38F/W44F, taken together with the detailed structural information available for barstar, provide a possible explanation for the unusual emission spectrum of C5 protein.

L27 ANSWER 11 OF 13 CAPLUS COPYRIGHT 2002 ACS
1997:135161 Document No. 126:250048 Characterization of two scleroderma autoimmune antigens that copurify with human ***ribonuclease*** ***P*** . ***Eder, Paul S.*** ; Kekuda, Ramesh; Stolc, Viktor; Altman, Sidney (Dep. Biology, Yale Univ., New Haven, CT, 06520, USA). Proc. Natl. Acad. Sci. U. S. A., 94(4), 1101-1106 (English) 1997. CODEN: PNASA6. ISSN: 0027-8424. Publisher: National Academy of Sciences.
AB Human ***RNase*** ***P*** has been purified more than 2000-fold from HeLa cells. In addn. to the RNA component, H1 RNA, polypeptides of mol. masses 14, 20, 25, 30, 38, and 40 kDa copurify with the enzyme activity. Sera from two different patients with the autoimmune disease scleroderma were used to immunodeplete human ***RNase*** ***P*** activity. These same sera cross-reacted on immunoblots with two of the copurifying polypeptides, p30 and p38, whereas an autoimmune serum that does not immunodeplete ***RNase*** ***P*** activity did not react with these proteins. Peptide fragments derived from purified p30 and p38 facilitated the mol. cloning and sequencing of cDNAs coding or these two polypeptides, which are now designated as Rpp30 and Rpp38, resp. RPP38 cDNA encodes a polypeptide that may be identical to a previously identified antigen of .apprxeq.40 kDa, which is immunopptd. by Th and To autoimmune antisera, and that has been implicated as a protein subunit of human ***RNase*** ***P*** by virtue of its ability to bind to H1 RNA in vitro. The second autoimmune antigen, Rpp30, as such, has not been described previously.

L27 ANSWER 12 OF 13 CAPLUS COPYRIGHT 2002 ACS
1996:541905 Document No. 125:215576 The RNA subunit of ***ribonuclease*** ***P*** from the zebrafish, Danio rerio. ***Eder, Paul S.*** ;

Srinivasan, Ashok; Fishman, Mark C.; Altman, Sidney (Dep. Biol., Yale Univ., New Haven, CT, 06520, USA). J. Biol. Chem., 271(35), 21031-21036 (English) 1996. CODEN: JBCHA3. ISSN: 0021-9258.

AB A simple strategy has been devised to identify the gene encoding the RNA subunit of ***RNase*** ***P*** from the zebrafish, CAnio rerio. The sequence obtained by amplification of genomic DNA with primers based on sequences common to two other vertebrates was confirmed by reverse transcription and amplification of RNA from a partially purified prepn. of the holoenzyme. The 5' and 3' ends were detd. by cyclizing the RNA, followed by reverse transcription and sequencing across the ligated RNA junction. The zebrafish sequence is 63% identical to that of Xenopus laevis nuclear ***RNase*** ***P*** RNA and 69% identical to the human ***RNase*** ***P*** RNA. A consensus secondary structure was constructed based on these nucleotide identities and on the many compensatory base changes in several regions among these three RNAs. The strategy used to obtain the zebrafish sequence should be useful in deriving analogous gene sequences from diverse classes of eukaryotes.

L27 ANSWER 13 OF 13 CAPLUS COPYRIGHT 2002 ACS

1996:73959 Document No. 124:139265 RNA-protein interactions in ***RNase*** ***P*** . ***Gopalan, Venkat*** ; Talbot, Simon J.; Altman, Sidney (Department Biology, Yale University, New Haven, CT, 06520, USA). RNA-Protein Interact., 103-26. Editor(s): Nagai, Kiyoshi; Mattaj, Iain W. IRL Press: Oxford, UK. (English) 1994. CODEN: 62HLAM.

AB A review, with 71 refs. Topics discussed include the effects elicited by C5 protein when present as part of the ***RNase*** ***P*** holoenzyme (M1 RNA plus C5 protein).

	L #	Hits	Search Text	DBs
1	L1	225	RNASE ADJ P	USPAT ; US-PG PUB
2	L2	135	RIBONUCLEASE ADJ P	USPAT ; US-PG PUB
3	L3	46712	ANTIBIOTIC	USPAT ; US-PG PUB
4	L4	22593	ANTIBACTERIAL	USPAT ; US-PG PUB
5	L5	6092	CONSENSUS ADJ SEQUENCE	USPAT ; US-PG PUB
6	L6	299	L1 OR L2	USPAT ; US-PG PUB
7	L7	120	L6 AND L3	USPAT ; US-PG PUB
8	L8	4	L6 SAME L3	USPAT ; US-PG PUB
9	L9	78	L6 AND L5	USPAT ; US-PG PUB
10	L10	1	L6 SAME L5	USPAT ; US-PG PUB
11	L11	5	L8 OR L10	USPAT ; US-PG PUB